

		*****	* * *	** *****	* *****	**
Plant	At	FYKVEAIVRP	WRIQQVSSAL	LKIGIRGVTV	SDVRGFGAOG	
	Ric	FYKVEAILRP	WRVSOVSSAL	LKIGIRGVTV	SDVRGFGAOG	
	Kp	MKKIDAIKIP	FKLDDVREAL	AEVGITGMTV	TEVKGFGROK	
	Ec	MKKIDAIKIP	FKLDDVREAL	AEVGITGMTV	TEVKGFGROK	
	RL	MKKIEAIKIP	FKLDEV-SP	SGVGLOGITV	TEAKGFGROK	
Bacteria	Bj	MKKIEAIKIP	FKLDEV-SL	SGVGLOGITV	TEAKGFGROK	
	Az	MKKIEAIKIP	FKLDEVKEAL	HEVGIGKITV	TEAKGFGROK	
	Rc	MKKVEAIKIP	FKLDEVKEAL	QEAGIOGLSV	IEVKGFGROK	
	Sy	MKKIEAIIRP	FKLDEVKIAL	VNAGIVGMTV	SEVRGFGROK	
Archaeobacteria	Mt1	MKMIKAIVRP	DKVDDIVDSL	ENAGYPAFTK	INSVGRGKOG	
	Mt2	MKEVIAIIRP	NTVSKTVKAL	DVVGFPVMTM	AECFGRGKOK	
		1	↓			
		* **	*** *	* * *	** *****	** ** *
Plant	At	GSTERHGGSE	FSEDKFVAKV	KMEIVVKKDQ	VESVINTIIE	
	Ric	GSTERQGGSE	FSEDKFVAKV	KMEIVVSKDQ	VEDVIEKIIE	
	Kp	GHTELYRGAE	YMVD-FLPKV	KIEIVVTDDI	VDTCDVTIIR	
	Ec	GHTELYRGAE	YMVD-FLPKV	KIEIVVPDDI	VDTCDVTIIR	
	RL	GHTELYRGAE	YVVD-FLPKV	KVEVVLADEN	AEAVIEAIRK	
Bacteria	Bj	GHTDLYTGAE	YIVD-FLPKV	KIEIVIGDDL	VERAIDAIIR	
	Az	GHTELYRGAE	YVVD-FLPKV	KIEVVMEDSL	VERAIEAIQQ	
	Rc	GHTELYRGAE	YVVD-FLPKV	KIEMVLPDEM	VDIAIEAIVG	
	Sy	GOTERYRGSE	YTVE-FLOKL	KLEIVVEDAQ	VDTVIDKIVA	
Archaeobacteria	Mt1	GLKVGE---I	FY-D-ELPKT	ILLIAVNDDE	VDEVVGLIKS	
	Mt2	GYEEGEKEGR	FIK--YIPKR	LISIVVDDAD	VPLVVGIISK	
		51	↓			
		*****	*****	* *****	** *	*
Plant	At	GARTGEIGDG	KIFVLPVSDV	IRVRTGERGE	KAE	
	Ric	EARTGEIGDG	KIFLLPVSDV	IRVRTGERGD	KAE	
	Kp	TAQTGKIGDG	KIFVFDVARV	IRIRTGEEDD	AAI	
	Ec	TAQTGKIGDG	KIFVFDVARV	IRIRTGEEDD	AAI	
	RL	AAQTGRIGDG	KIFVSNVEEV	IRIRTGETGI	DAI	
Bacteria	Bj	AAQTGRIGDG	KIFVSNIEEA	IRIRTGESGL	DAI	
	Az	AAHTGRIGDG	KIFVTPVEEV	VRIRTGEKGG	DAI	
	Rc	AARTEKIGDG	KIFVSSIEQA	IRIRTGETGE	DAV	
	Sy	AARTGEIGDG	KIFVSPVDQT	IRIRTGEKNA	DAI	
Archaeobacteria	Mt1	SASTGNFGDG	KIFIQPI TEA	YTIRTGETGI	---	
	Mt2	VNRTGSFGDG	RIFVLPVEEA	IRVRTGETGE	IAI	
		112				

FIG. 1A

5914089

2 of 13

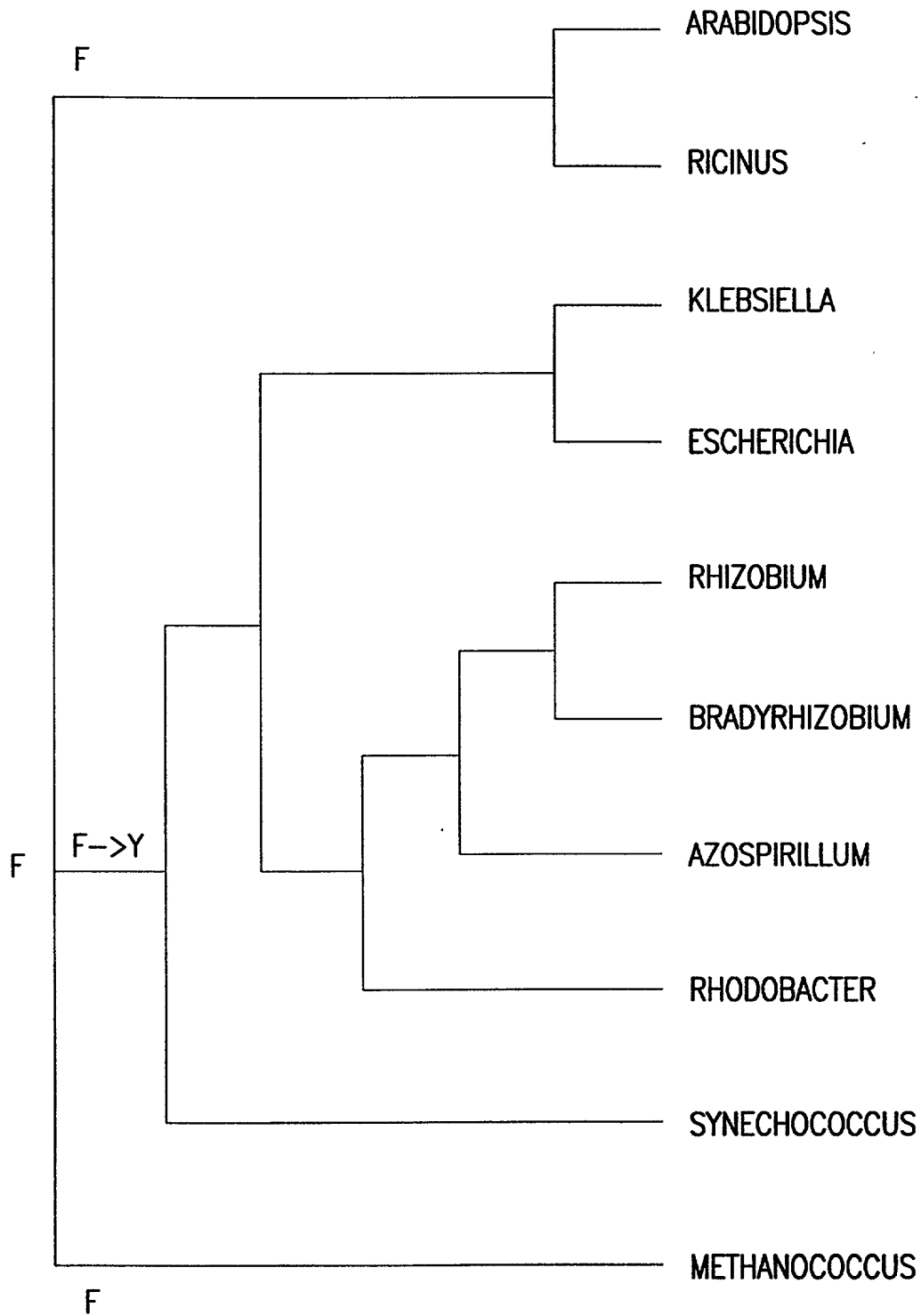


FIG. 1B

5914089

3 of 13

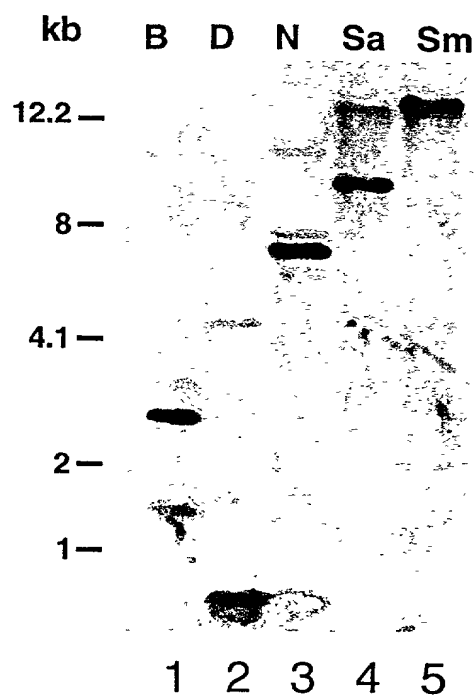


FIG.2

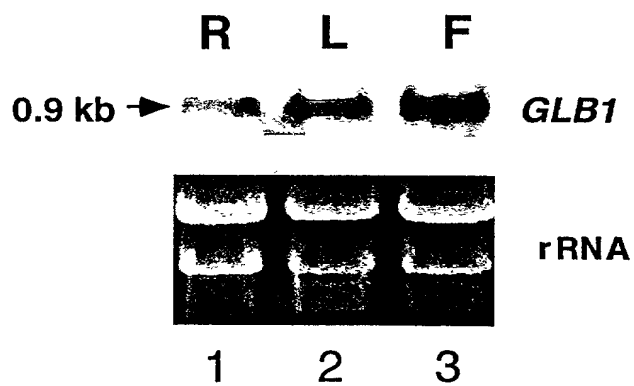


FIG.3

5914 089

4 of 13

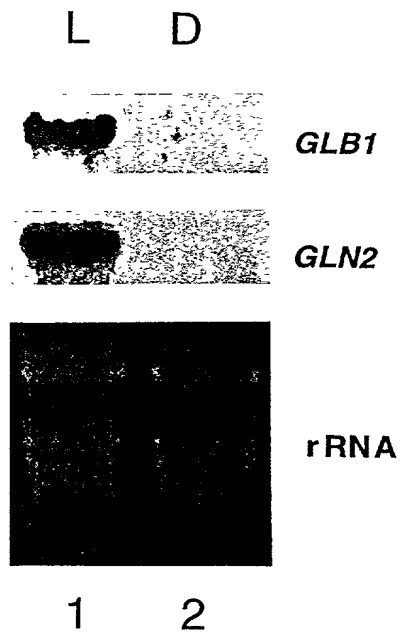


FIG.4A

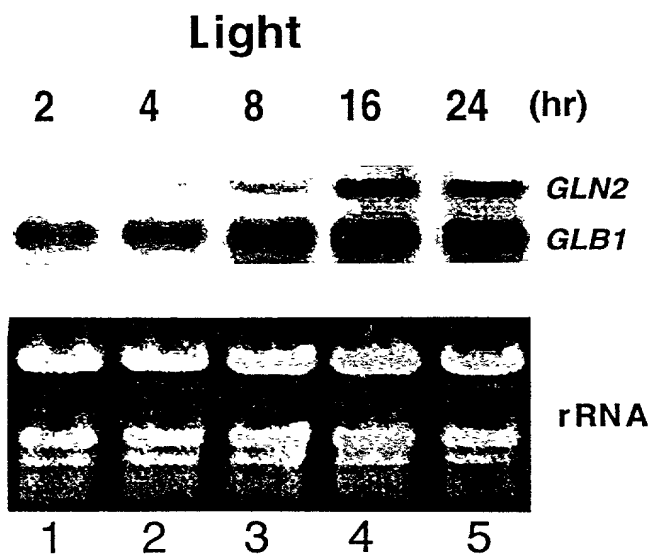


FIG.4B

5914089

5 of 13

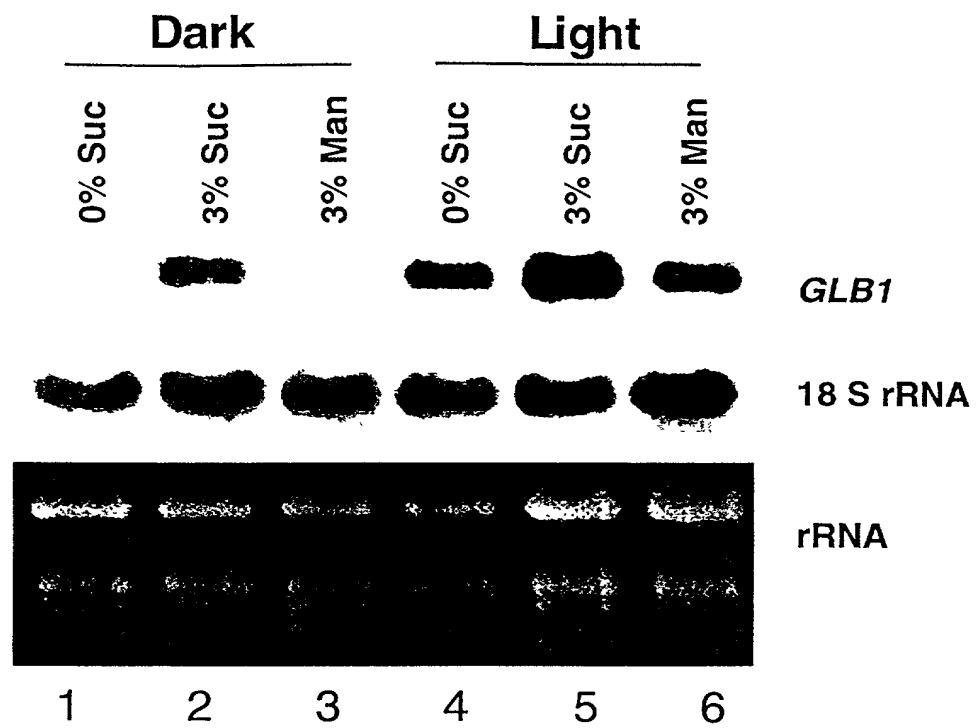


FIG.5

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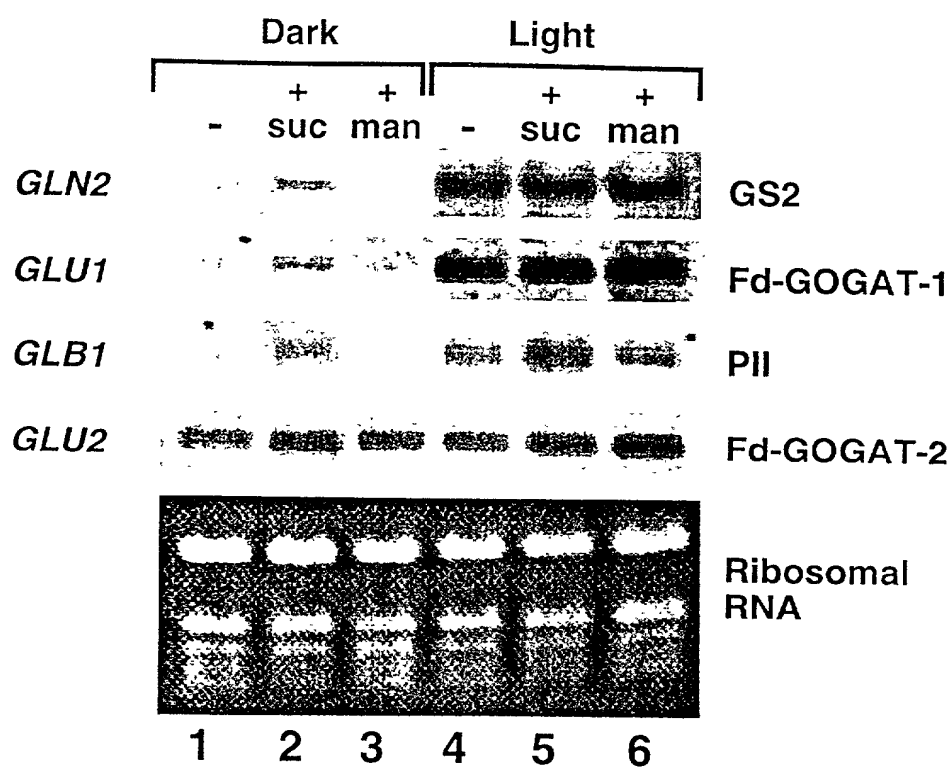


FIG.6

5914089

7 of 13

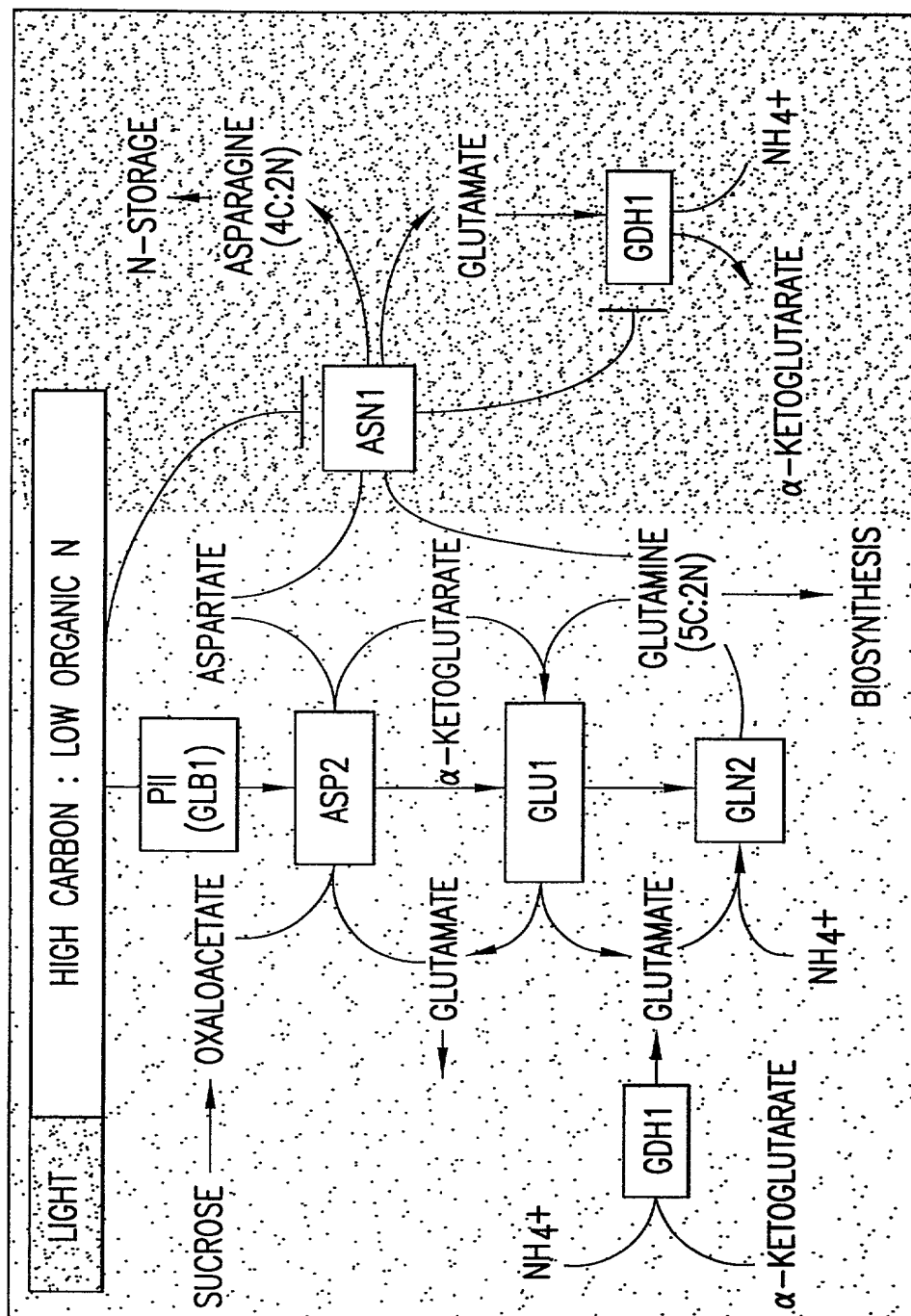


FIG.7

5914089

8 of 13

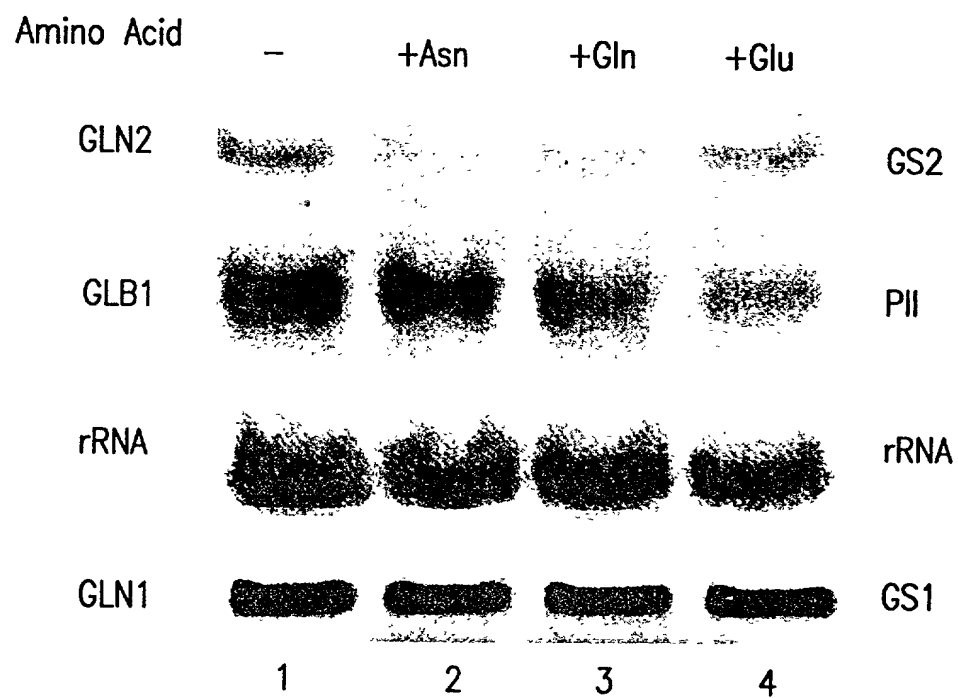


FIG.8



5914089

9 of 13

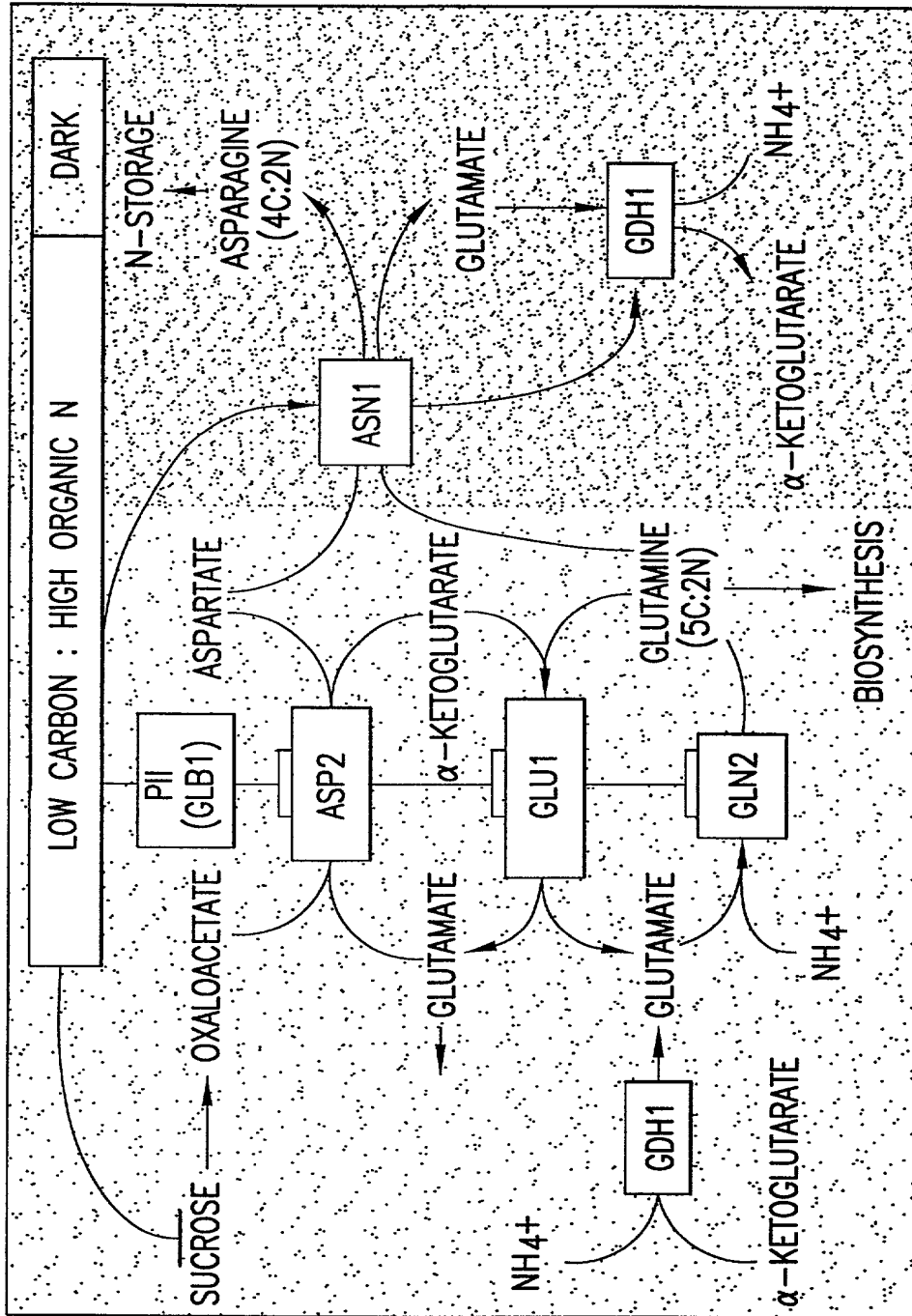


FIG.9

5914089

10 of 13

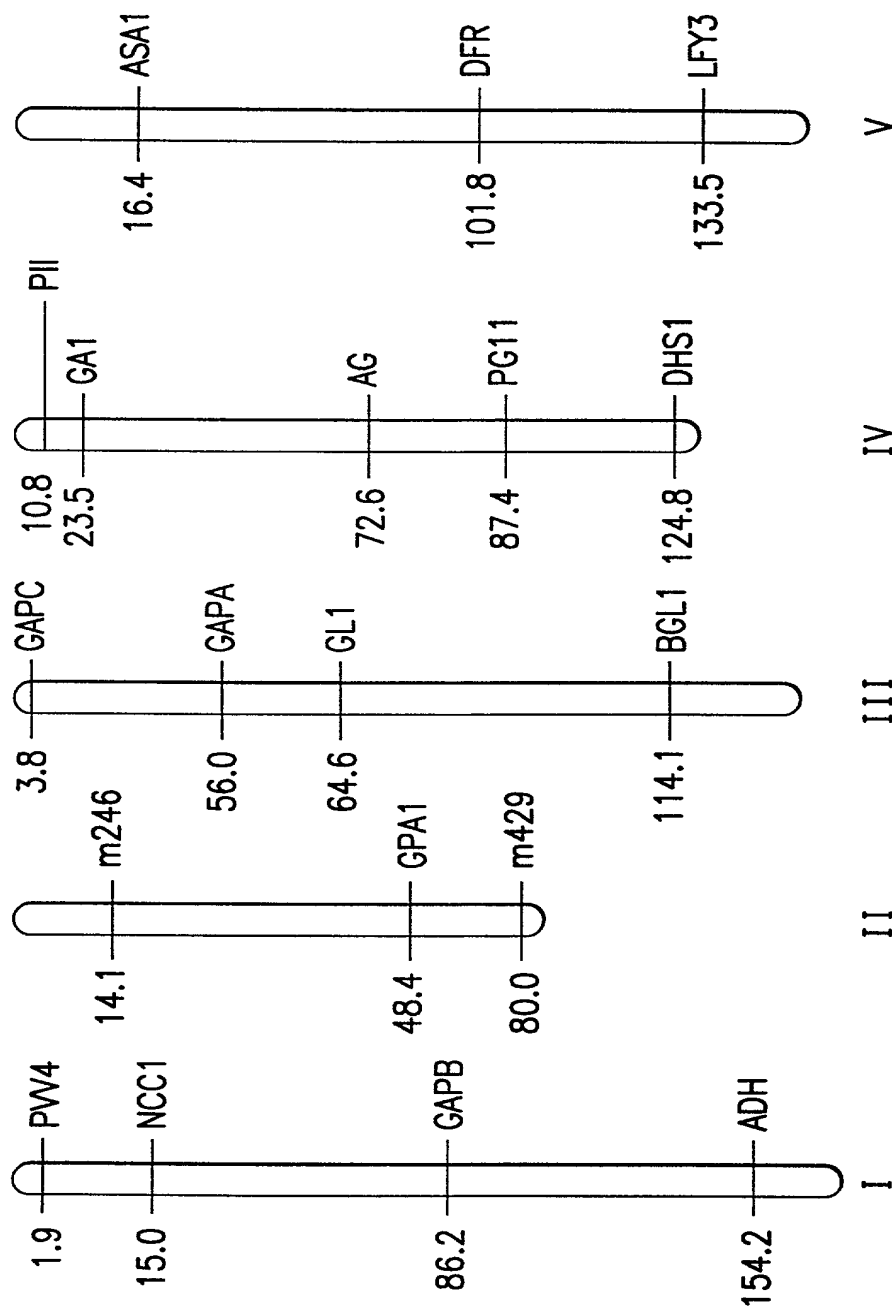


FIG.10

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11 413

1 ctgaaagttg tgttaaaaaa aaaactagaa tcatggcggc gtcaatgacg  
51 aaacccatct caataacttc tctcggtttc tattctgacg gaaagaacat  
101 tgctttctct gattgcattt cgatttggtc tggattcaga cattcccac  
151 catcttgccg cgatttggtc acaaagtcac cgagtaataa cagtcgtgtt  
201 ttacctgtcg ttagtgccca aatatcttct gattatattc cagactcgaa  
251 attttacaag gtggaagcaa ttgtcagacc atggagaatc cagcaagttt  
301 catcggcttt actgaaaatc gggattcgag gtgttactgt ttctgatgtg  
351 agagggtttg gtgcacaagg aggttctacc gagagacacg gtggctctga  
401 gttctcggaa gacaaatttg ttgctaaagt taagatggaa atcgttgta  
451 agaaagacca agtggaatct gtaatcaaca caataattga aggagcaagg  
501 acaggagaga ttggtgatgg caagattttt gttttgcctg tgtcagatgt  
551 cataagagtt aggacagggtg agcgtgggga gaaagcagag aagatgactg  
601 gtgatatgct ttcaccgtct taggaacaaa cagagctcaa gaatggtttt  
651 ttttttttct atttcgggtc ctagattctg cgaataataa tgaatggagt  
701 ctgtgtttgg tttcatgttg aatcgatcaa gatgtgtttt taactgtaca  
751 tgaattatgc agaaacatct gtcctgggtc tcagacatcg aaactctgtt  
801 cctaataaaa aaaaaaa

FIG. 12

5914089

12 of 13

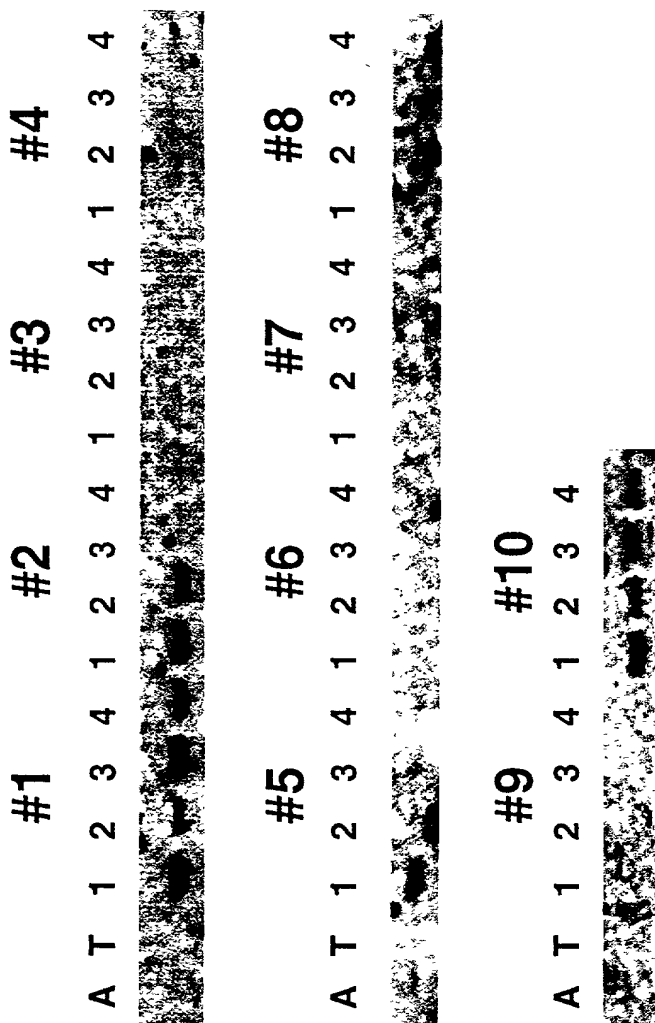


FIG.11

1 GCGGTGTCGG CCGCTCTAGA ACTAGTGGAT CCCCCGGGCT GCAGGAATTC  
51 GGCACGAGGC TACTGCGAAA CTGGGCTTGC TCACTCCTCT TCATTCTAAT  
101 AACATCAAGA AAGAATTCCC TGTTTTTGAT TTCAGTTTGT TTTGTCCAGA  
151 GCTTAGACAT TCTCGGTTTT CTCAC TTAA CACCGCGGTC AAGCGCGTAA  
201 GATATGCCCC CGTCGTTCTT GTGATTAATG CCCAAAGCTC GCCTGACTAC  
251 ATTCCTGATG CTAAATTCTA CAAAGTGGAA GCAATTCTCA GGCCCTGGCG  
301 AGTCTCGCAA GTTTCCTCGG CTTTGCTAAA AATTGGTATT CGAGGTGTTA  
351 CTGTTTCTGA TGTTGAGGT TTTGGTGCTC AAGGTGGTTC AACTGAGAGG  
401 CAGGGCGGCT CAGAATTTTC TGAAGACAAG TTTGTTGCTA AAGTTAAGAT  
451 GGAGATCGTG GTTAGCAAAG ACCAGGTTGA GGATGTTATA GAAAAAATCA  
501 TTGAGGAGGC AAGAACTGGA GAGATTGGAG ACGGCAAGAT TTTCTTGCTG  
551 CCTGTTTCAG ATGTAATAAG AGTCCGCACT GGTGAGCGGG GTGATAAGGC  
601 TGAGAGGATG ACAGGAGGGC GATCTGACAT GAGTACTTCT GCTTGACTGC  
651 TGTGACCAGC AATATAGCAT TCAGGACTAA CTGTCCTTTG AGAAAGCCCC  
701 GCCCTTATTA GCCATTATCC AGTATAGCTT GATAATTTGA ATTTTTTGT  
751 TTCTTAACTA AAGAAACAAA GATCTTTTCA TTATCCTGTT GATGATAATT  
801 GAAAACGGAA GGATCGCGAA TTTGTTCAAG TGCTTGCAAG ATAAATAACA  
851 AGAAGAGGAG TAATGTTAAC AAAAAAAAAA AAAAAAAAAA ACTCGAG

FIG.13